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SEQUENCE LISTING

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<120> GENE CODING FOR HELIOMICINE, AND USE THEREOF

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<160> 38

<170> PatentIn Ver. 2.1

<210> 1

<211> 147

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<222> (1)..(147)

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agc ttg gat aaa aga gac aag ttg att ggc agc tgt gtt tgg ggc gcc
 48

Ser Leu Asp Lys Arg Asp Lys Leu Ile Gly Ser Cys Val Trp Gly Ala
 1 5 10 15

gtc aac tac act agt gac tgc aac ggc gag tgc aag cgc cgc ggt tac
 96

Val Asn Tyr Thr Ser Asp Cys Asn Gly Glu Cys Lys Arg Arg Gly Tyr
 20 25 30

aag ggt ggc cat tgt gga tcc ttc gct aac gtt aac tgt tgg tgt gaa
 144

Lys Gly Gly His Cys Gly Ser Phe Ala Asn Val Asn Cys Trp Cys Glu
 35 40 45

acc
147
Thr

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<220>
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<222> (1)..(132)

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48
Asp Lys Leu Ile Gly Ser Cys Val Trp Gly Ala (Val) Asn Tyr Thr Ser
1 5 10 15

gat tgc aac ggt gag tgc aag agg agg ggt tac aag ggt ggt cac tgc
96
Asp Cys Asn Gly Glu Cys Lys Arg Arg Gly Tyr Lys Gly Gly (His) Cys
20 25 30

ggt tcc ttc gct aac gtg aac tgc tgg tgc gag act tgagagctcg
142
Gly Ser Phe Ala Asn (Val) Asn Cys Trp Cys Glu Thr
35 40

gcgaggcgaa cgtgtcgacg gatccgg
169

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<222> (3)..(224)

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47
Met Gly Phe Val Leu Phe Ser Gln Leu Pro Ser Phe Leu Leu Val

1 5 10 15
 tct act ctt ctt ctt ttc ctt gtg atc tct cac tct tgc cgt gcc gat
 95
 Ser Thr Leu Leu Leu Phe Leu Val Ile Ser His Ser Cys Arg Ala Asp
 20 25 30
 aag ctt atc ggt tcc tgc gtg tgg ggt gct gtg aac tac act tcc gat
 143
 Lys Leu Ile Gly Ser Cys Val Trp Gly Ala Val Asn Tyr Thr Ser Asp
 35 40 45
 tgc aac ggt gag tgc aag agg agg ggt tac aag ggt ggt cac tgc ggt
 191
 Cys Asn Gly Glu Cys Lys Arg Arg Gly Tyr Lys Gly Gly His Cys Gly
 50 55 60
 tcc ttc gct aac gtg aac tgc tgg tgc gag act tgagagctcg gcgaggcgaa
 244
 Ser Phe Ala Asn Val Asn Cys Trp Cys Glu Thr
 65 70
 cgtgtcgacg gatccgg
 261
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 <222> (12)..(101)
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 50
 Met Gly Phe Val Leu Phe Ser Gln Leu Pro Ser Phe Leu
 1 5 10
 ctt gtg tct act ctt ctt ctt ttc ctt gtg atc tct cac tct tgc cgt
 98
 Leu Val Ser Thr Leu Leu Leu Phe Leu Val Ile Ser His Ser Cys Arg
 15 20 25
 gct ggagacgcga attcacaca
 120

Ala
30

<210> 5
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gcgtcgacgc gatgggtttc gtgcttttct ctcagcttcc atctttcctt cttgtgtcta
60

ctctttcttct ttcc
75

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tcgccggcac ggcaagagta agagatcaca aggaaaagaa gaagagtaga cacaagaagg
60

aaagatggaa gc
72

<210> 7
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60

gagtgcaga ggaggggtta
80

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<400> 8
ccggatccgt cgacacgttc gcctcgccga gctctcaagt ctgcaccag cagttcacgt
60

tagcgaagga accgcagtga ccacccttgt aaccctcct cttgcactc
109

<210> 9
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agggcccccct agggtttaaa cggccagtca ggccgaattc gagctcggtta cccgggggatac
60

ctctagagtc gacctgcagg catgc
85

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<212> ADN
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ccctgaacca ggctcgaggg cgcgccttaa ttaaaagctt gcatgcctgc aggtcgactc
60

tagagg
66

<210> 11
<211> 93
<212> ADN
<213> synthetic construct

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60

gctcgagggc ccaacctcag tacctgggtc agg
93

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gcgtttaaac ttaattaagt gtggcctgac tgg
 93

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<210> 14
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 <222> (7)..(72)

<400> 15
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 48

Met Ala Cys Thr Asn Asn Ala Met Arg Ala Leu Phe Leu Leu
 1 5 10

ctg ctc ttc tgc atc gtg cac ggc gccgaattc

81

Leu Leu Phe Cys Ile Val His Gly
 15 20

<210> 16

<211> 24

<212> ADN

<213> synthetic construct

<400> 16

gataagctta tcggttcctg cgtg
 24

<210> 17

<211> 32

<212> ADN

<213> synthetic construct

<400> 17

ggctcagagtc aagtctcgca ccagcagttc ac
 32

<210> 18

<211> 213

<212> ADN

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<220>

<221> CDS

<222> (7)..(204)

<400> 18

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 48

Met Ala Cys Thr Asn Asn Ala Met Arg Ala Leu Phe Leu Leu
 1 5 10

ctg ctc ttc tgc atc gtg cac ggc gat aag ctt atc ggt tcc tgc gtg
 96

Leu Leu Phe Cys Ile Val His Gly Asp Lys Leu Ile Gly Ser Cys Val
 15 20 25 30

tgg ggt gct gtg aac tac act tcc gat tgc aac ggt gag tgc aag agg
 144

Trp Gly Ala Val Asn Tyr Thr Ser Asp Cys Asn Gly Glu Cys Lys Arg

35

40

45

agg ggt tac aag ggt ggt cac tgc ggt tcc ttc gct aac gtg aac tgc
 192
 Arg Gly Tyr Lys Gly Gly His Cys Gly Ser Phe Ala Asn Val Asn Cys
 50 55 60

tgg tgc gag act tgactcgag
 213
 Trp Cys Glu Thr
 65

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<220>
 <221> promoter
 <222> (7)..(532)

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 <222> (533)..(568)

<220>
 <221> terminator
 <222> (569)..(832)

<400> 19
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actatggaag tattatgtga gctcagcaag aagcagatca atatgaggca catatgcaac
 120

ctatgttcaa aaatgaagaa tgtacagata caagatccta tactgccaga atacgaagaa
 180

gaatacgtag aaattgaaaa agaagaacca ggcaagaaa agaattctga agacgtaagc
 240

actgacgaca acaatgaaaa gaagaagata aggtcgggtga ttgtgaaaga gacatagagg
 300

acacatgtaa ggtggaaaat gtaagggcgg aaagtaacct tatcaciaag gaatcttacc
 360

ccccactact taccctttta tatttttccg tgtcattttt gcccttgagt tttcctatat
420

aaggaaccaa gttcggcatt tgtgaaaaca agaaaaaatt tgggtgaagc tattttcttt
480

gaagtactga ggatacaact tcagagaaat ttgtaagttt gtagatctcg attctagaag
540

gcctgaattc gagctcggta ccggatccaa ttcccgatcg ttcaaacatt tggcaataaa
600

gtttcttaag attgaatcct gttgccggtc ttgcgatgat tatcatataa tttctgttga
660

attacgttaa gcatgtaata attaacatgt aatgcatgac gttatttatg agatggggtt
720

ttatgattag agtcccgcaa ttatacattt aatacgcgat agaaaacaaa atatagcgcg
780

caaactagga taaattatcg cgcgcgggtgt catctatggt actagatcgg ggatcgat
838

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<212> ADN
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<222> (539)..(736)

<220>
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<222> (767)..(1030)

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120

ctatgttcaa aaatgaagaa tgtacagata caagatccta tactgccaga atacgaagaa
180

gaatacgtag aaattgaaaa agaagaacca ggcgaagaaa agaattctga agacgtaagc
240

actgacgaca acaatgaaaa gaagaagata aggtcgggtga ttgtgaaaga gacatagagg
300

acacatgtaa ggtggaaaaat gtaagggcgg aaagtaacct tatcaciaag gaatcttacc
360

ccccactact taccctttta tttttttccg tgtcattttt gcccttgagt tttcctatat
420

aaggaaccaa gttcggcatt tgtgaaaaca agaaaaaatt tgggtgaagc ttttttcttt
480

gaagtactga ggatacaact tcagagaaat ttgtaagttt gtagatctcg attctaga
538

atg gcc tgc acc aac aac gcc atg agg gcc ctc ttc ctc ctc gtg ctc
586
Met Ala Cys Thr Asn Asn Ala Met Arg Ala Leu Phe Leu Leu Val Leu
1 5 10 15

ttc tgc atc gtg cac ggc gat aag ctt atc ggt tcc tgc gtg tgg ggt
634
Phe Cys Ile Val His Gly Asp Lys Leu Ile Gly Ser Cys Val Trp Gly
20 25 30

gct gtg aac tac act tcc gat tgc aac ggt gag tgc aag agg agg ggt
682
Ala Val Asn Tyr Thr Ser Asp Cys Asn Gly Glu Cys Lys Arg Arg Gly
35 40 45

tac aag ggt ggt cac tgc ggt tcc ttc gct aac gtg aac tgc tgg tgc
730
Tyr Lys Gly Gly His Cys Gly Ser Phe Ala Asn Val Asn Cys Trp Cys
50 55 60

gag act tgactcgagg gggggcccggt taccggatcc aattcccgat cgttcaaaca
786
Glu Thr
65

tttggcaata aagtttctta agattgaatc ctgttgccgg tcttgcatg attatcatat
846

aatttctgtt gaattacgtt aagcatgtaa taattaacat gtaatgcatg acgttattta
906

tgagatgggt ttttatgatt agagtcccg c aattatacat ttaatacgcg atagaaaaca
966

aaatatagcg cgcaaactag gataaattat cgcgcgcggt gtcactatg ttactagatc
1026

ggggatcgat
1036

<210> 21
<211> 52
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52

<210> 22
<211> 56
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<213> synthetic construct

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56

<210> 23
<211> 52
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<213> synthetic construct

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actacactag tgactgcaac ggcgagtgc agcgccgcgg ttacaagggt gg
52

<210> 24
<211> 52

<212> ADN

<213> synthetic construct

<400> 24

cacaatggcc acccttgtaa ccgcggcgct tgcactcgcc gttgcagtca ct
52

<210> 25

<211> 56

<212> ADN

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<400> 25

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56

<210> 26

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52

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42

<210> 28

<211> 42

<212> ADN

<213> synthetic construct

<400> 28

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42

<210> 29
<211> 32
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<400> 29
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32

<210> 30
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<213> synthetic construct

<400> 30
gcaacaagca ctcgccgttg cagtca
26

<210> 31
<211> 32
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32

<210> 32
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<400> 32
gccgcttgca ctcagcagcg cagtca
26

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40

<210> 34
<211> 18
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ggggcgccgt caactaca
18

<210> 35
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<400> 35
ctagtgtagt tgacggcgcc cc
22

<210> 36
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<400> 36
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36

<210> 37
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32

<210> 38
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<213> synthetic construct

<400> 38

gcaacaagca ctcagcagcg cagtca
26